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ID DLK2_HUMAN Reviewed; 383 AA.
 AC Q6UYI1; Q5T3T8; Q9BQ54;
 DT 25-OCT-2004, integrated into UniProtKB/Swiss-Prot.
 DT 05-JUL-2004, sequence version 1.
 DT 22-JUL-2008, entry version 48.
 DE RecName: Full=Delta-like protein 2;
 DE AltName: Full=EGF-like domain-containing protein 9;
 DE AltName: Full=Multiple EGF-like domain protein 9;
 DE Flags: Precursor;
 GN Name=DLK2; Synonyms=EGFL9; ORFNames=UNQ2903/PRO28633;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorh
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RX MEDLINE=22687296; PubMed=12975309; DOI=10.1101/gr.129800.
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T.
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., He
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Le
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Sch
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J.
 RA Vanden R.L., Watanabe C., Wieand D., Woods K., Xie M.-H
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z.,
 RA Wood W.I., Godowski P.J., Gray A.M.;
 RT "The secreted protein discovery initiative (SPDI), a large
 RT effort to identify novel human secreted and transmembrane
 RL bioinformatics assessment."; Genome Res. 13:2265-2270(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=22935763; PubMed=14574404; DOI=10.1093/nar/gkq000.
 RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashu
 RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.
 RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscow
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.
 RA Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barl
 RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O
 RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown
 RA Burford D.C., Burrill W., Burton J., Carder C., Carter N
 RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S.,
 RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Cov
 RA Cully K.M., Dhani P., Davies J., Dunn M., Earthrow M.E.
 RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., F
 RA Frankland J., French L., Garner P., Garnett J., Ghorri M.
 RA Gilby L.M., Gillson C.J., Glithero R.J., Graham D.V., G
 RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Hal
 RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcot
 RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle
 RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M.,
 RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K.

RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R.,
 RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi
 RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McL

 RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Ni
 RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Pa
 RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S.
 RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T.
 RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M.,
 RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G.,
 RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans
 RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S
 RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.I
 RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulso
 RA Durbin R.M., Hubbard T., Sulston J.E., Dunham I., Rogers
 RT "The DNA sequence and analysis of human chromosome 6."
 RL Nature 425:805-811(2003).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2
 RC TISSUE=Eye;
 RX PubMed=15499334; DOI=10.1101/gr.2596504;
 RG The MGC Project Team;
 RT "The status, quality, and expansion of the NIH full-length
 RT project: the Mammalian Gene Collection (MGC).";
 RL Genome Res. 14:2121-2127(2004).
 CC -!- SUBCELLULAR LOCATION: Membrane; Single-pass type I m
 CC protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q6UY11-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q6UY11-2; Sequence=VSP_011767;
 CC Note=Splicing acceptor site not canonical. No exper
 CC confirmation available;
 CC -!- SIMILARITY: Contains 6 EGF-like domains.
 CC -----
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 CC -----
 DR EMBL: AY359126; AAQ88493.1; -; mRNA.
 DR EMBL: AL2359813; CAI23224.1; -; Genomic_DNA.
 DR EMBL: BC000230; AAR00230.1; -; mRNA.
 DR EMBL: BC006425; AAR06425.1; -; mRNA.
 DR EMBL: BC110320; AAI10321.1; -; mRNA.
 DR RefSeq: NP_076421.2; -.
 DR RefSeq: NP_996262.1; -.
 DR UniGene: Hs.237251; -.
 DR Ensembl: ENSG00000171462; Homo sapiens.
 DR GeneID: 65989; -.
 DR KEGG: hsa:65989; -.
 DR H-InvDB: HIX000594; -.
 DR HGNC: HGNC:21113; DLK2.
 DR PharmGKB: P313522183; -.
 DR HOGENOM: Q6UY11; -.
 DR HOVERGEN: Q6UY11; -.
 DR CleanEx: AS_DLK2; -.
 DR GermOnline: ENSG00000171462; Homo sapiens.
 DR InterPro: IPR006210; EGF.
 DR InterPro: IPR000152; EGF-type_Asp/Asn_hydroxyl_CS.
 DR InterPro: IPR001439; EGF_2.
 DR InterPro: IPR000742; EGF_3.
 DR InterPro: IPR001821; EGF_Ca_bd.
 DR InterPro: IPR000000; EGF_1_5.

DR INTERPRO; [IPR000008](#); EGF_like.
 DR InterPro; [IPR013032](#); EGF_like_reg_CS.
 DR Pfam; [PF00008](#); [EGF](#); 5.

DR PRINTS; [PR00010](#); EGFBL00D.
 DR SMART; [SM00181](#); EGF; 3.
 DR SMART; [SM00175](#); EGF_CA; 2.
 DR PROSITE; [PS00010](#); ASX_HYDROXYL; 2.
 DR PROSITE; [PS00022](#); EGF_1; 6.
 DR PROSITE; [PS01186](#); EGF_2; 6.
 DR PROSITE; [PS00026](#); EGF_3; 6.
 DR PROSITE; [PS01187](#); EGF_CA; 2.
 PE 2: Evidence at transcript level;
 KW Alternative splicing; Calcium; EGF-like domain; Glycoprotein; Repeat; Signal; Transmembrane.

FT	SIGNAL	1	26	Potential.
FT	CHAIN	27	383	Delta-like protein 2.
FT				/FTId=PRO_0000007531.
FT	TOPO_DOM	27	306	Extracellular (Potential).
FT	TRANSMEM	307	327	Potential.
FT	TOPO_DOM	328	383	Cytoplasmic (Potential).
FT	DOMAIN	27	58	EGF-like 1.
FT	DOMAIN	62	89	EGF-like 2.
FT	DOMAIN	91	129	EGF-like 3.
FT	DOMAIN	131	172	EGF-like 4.
FT	DOMAIN	174	210	EGF-like 5; calcium-binding
FT	DOMAIN	212	248	EGF-like 6; calcium-binding
FT	CARBOHYD	157	157	N-linked (GlcNAc...) (Potential)
FT	DISULFID	29	40	By similarity.
FT	DISULFID	33	46	By similarity.
FT	DISULFID	48	57	By similarity.
FT	DISULFID	66	71	By similarity.
FT	DISULFID	79	88	By similarity.
FT	DISULFID	95	107	By similarity.
FT	DISULFID	101	117	By similarity.
FT	DISULFID	119	128	By similarity.
FT	DISULFID	135	148	By similarity.
FT	DISULFID	142	160	By similarity.
FT	DISULFID	162	171	By similarity.
FT	DISULFID	178	189	By similarity.
FT	DISULFID	183	198	By similarity.
FT	DISULFID	200	209	By similarity.
FT	DISULFID	216	227	By similarity.
FT	DISULFID	221	236	By similarity.
FT	DISULFID	238	247	By similarity.
FT	VAR_SEQ	1	179	Missing (in isoform 2).
FT				/FTId=VSE_011767.
SQ	SEQUENCE	383 AA;	40548 MW;	701AC6B043863EA7 CRC64;
	MPSSGCRCLHL	VCLLCILGAP	QGPVRADDCS	SHCDLAHGCC
	APDGSRCRDP	G		
	VRMPGQCQHG	CHQPWQCICH	SGWAGKFCDK	DEHICTTQSP
	CQNGGQCQMYD	G		
	PGFHGRDCER	KAGPCEQAGS	PCRNNGQCQD	DQGFALNFTC
	RCLVGFVGAR	C		
	RPCANGATCL	DGINRFSCLC	PEGFAGRFCT	INLDDCASRP
	CQRGARCRDR	V		
	GYGKTCCELV	LPVPDPPTTV	DTPLGPTSAV	VVPATGPAPH
	SAGAGLLRIS	V		
	GLGEPISVAL	VVFGALTAAL	VLATVLLTLR	AWRRGVCPPG
	PCCYPAPHYA	P		
	SMLPAGLPLP	RDLPPPEPKT	TAL	

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